In the primary source article “Mapping genes related to early onset major depressive disorder in Dagestan genetic isolates” discusses the new findings of genes related to early onset major depressive disorder within the Caucasian Russian ethnic population. The approach they used in their experiment was a molecular and statistical population-genetic approach.

Two diverse, multigenerational pedigrees with early onset major depressive disorder where studied. Within each pedigree the number of living cases of major depressive disorder, and suicide cases of major depressive disorder was collected. The first pedigree had 19 living cases and 11 suicide committed case, while the second pedigree had 30 living cases and 12 committed suicide cases. Using a computer, multipoint parametric linkage analyses was performed which allowed the analyzation of selected cases by Affymetrix 6.0 SNP arrays. This refined the contribution of the copy number variations to the major depressive disorder genes.

In their results they found 18 genomic regions with nominal linkage to major depressive disorder and within 12 of those 18 regions copy number variations were detected. These results support the idea of mapping genes of complex diseases can help in detecting and speeding up the search for susceptibility genes.

References

Bulayeva, K., et al. Turkish Journal of Psychiatry. ***Mapping genes related to early onset major depressive disorder in Dagestan genetic isolates.*** https://pubmed.ncbi.nlm.nih.gov/22949285/ (2012).